



ENTERED

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/521,195B

DATE: 07/03/2002 P.6
TIME: 14:04:33

Input Set : A:\06501-057001.txt

Output Set: N:\CRF3\07032002\I521195B.raw

3 <110> APPLICANT: Nezu, Jun-Ichi
 4 Oku, Asuka
 6 <120> TITLE OF INVENTION: TRANSPORTER GENES
 8 <130> FILE REFERENCE: 06501-057001
 10 <140> CURRENT APPLICATION NUMBER: 09/521,195B
 11 <141> CURRENT FILING DATE: 2000-03-07
 13 <150> PRIOR APPLICATION NUMBER: JP 10/156660
 14 <151> PRIOR FILING DATE: 1998-05-20
 16 <150> PRIOR APPLICATION NUMBER: JP 9/260972
 17 <151> PRIOR FILING DATE: 1997-09-08
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04009
 20 <151> PRIOR FILING DATE: 1998-09-07
 22 <160> NUMBER OF SEQ ID NOS: 33
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 551
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
 30 Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro
 31 1 5 10 15
 32 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 33 20 25 30
 34 Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
 35 35 40 45
 36 Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn
 37 50 55 60
 38 Asn Ser Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His Ser
 39 65 70 75 80
 40 Cys Ser Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly
 41 85 90 95
 42 Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser
 43 100 105 110
 44 Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Val
 45 115 120 125
 46 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asn Trp Lys Val Pro Leu
 47 130 135 140
 48 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Val Ser
 49 145 150 155 160
 50 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Ala Thr
 51 165 170 175
 52 Met Ala Val Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Ile Ser
 53 180 185 190
 54 Trp Glu Met Phe Thr Val Leu Phe Val Ile Val Gly Met Gly Gln Ile

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55          195          200          205
56 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Gly Lys
57      210          215          220
58 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
59 225          230          235          240
60 Val Gly Tyr Met Leu Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
61          245          250          255
62 Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Val Pro
63          260          265          270
64 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
65          275          280          285
66 Arg Phe Arg Glu Ala Glu Asp Ile Ile Gln Lys Ala Ala Lys Met Asn
67      290          295          300
68 Asn Thr Ala Val Pro Ala Val Ile Phe Asp Ser Val Glu Glu Leu Asn
69 305          310          315          320
70 Pro Leu Lys Gln Gln Lys Ala Phe Ile Leu Asp Leu Phe Arg Thr Arg
71          325          330          335
72 Asn Ile Ala Ile Met Thr Ile Met Ser Leu Leu Leu Trp Met Leu Thr
73          340          345          350
74 Ser Val Gly Tyr Phe Ala Leu Ser Leu Asp Ala Pro Asn Leu His Gly
75          355          360          365
76 Asp Ala Tyr Leu Asn Cys Phe Leu Ser Ala Leu Ile Glu Ile Pro Ala
77      370          375          380
78 Tyr Ile Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg Tyr Ile
79 385          390          395          400
80 Ile Ala Ala Val Leu Phe Trp Gly Gly Gly Val Leu Leu Phe Ile Gln
81          405          410          415
82 Leu Val Pro Val Asp Tyr Tyr Phe Leu Ser Ile Gly Leu Val Met Leu
83          420          425          430
84 Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val Phe Thr
85          435          440          445
86 Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly Val Thr
87      450          455          460
88 Ser Thr Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe Val Tyr
89 465          470          475          480
90 Leu Gly Ala Tyr Asn Arg Met Leu Pro Tyr Ile Val Met Gly Ser Leu
91          485          490          495
92 Thr Val Leu Ile Gly Ile Phe Thr Leu Phe Phe Pro Glu Ser Leu Gly
93          500          505          510
94 Met Thr Leu Pro Glu Thr Leu Glu Gln Met Gln Lys Val Lys Trp Phe
95      515          520          525
96 Arg Ser Gly Lys Lys Thr Arg Asp Ser Met Glu Thr Glu Glu Asn Pro
97      530          535          540
98 Lys Val Leu Ile Thr Ala Phe
99 545          550
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 2135
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens

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106 <220> FEATURE:
107 <221> NAME/KEY: CDS
108 <222> LOCATION: (147)..(1799)
110 <400> SEQUENCE: 2
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112 cttggggagc gcccagcta caagacactg tcctgagaac gctgtcatca cccgtagttg      120
113 caagtttcg agcggcagtg ggaagc atg cgg gac tac gac gag gtg atc gcc      173
114                               Met Arg Asp Tyr Asp Glu Val Ile Ala
115                               1           5
116 ttc ctg ggc gag tgg ggg ccc ttc cag cgc ctc atc ttc ttc ctg ctc      221
117 Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
118 10           15           20           25
119 agc gcc agc atc atc ccc aat ggc ttc aat ggt atg tca gtc gtg ttc      269
120 Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
121           30           35           40
122 ctg gcg ggg acc ccg gag cac cgc tgt cga gtg ccg gac gcc gcg aac      317
123 Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
124           45           50           55
125 ctg agc agc gcc tgg cgc aac aac agt gtc ccg ctg cgg ctg cgg gac      365
126 Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
127           60           65           70
128 ggc cgc gag gtg ccc cac agc tgc agc cgc tac cgg ctc gcc acc atc      413
129 Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
130           75           80           85
131 gcc aac ttc tcg gcg ctc ggg ctg gag ccg ggg cgc gac gtg gac ctg      461
132 Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu
133 90           95           100           105
134 ggg cag ctg gag cag gag agc tgc ctg gat ggc tgg gag ttc agc cag      509
135 Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
136           110           115           120
137 gac gtc tac ctg tcc acc gtc gtg acc gag tgg aat ctg gtg tgt gag      557
138 Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
139           125           130           135
140 gac aac tgg aag gtg ccc ctc acc acc tcc ctg ttc ttc gta ggc gtg      605
141 Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
142           140           145           150
143 ctc ctc ggc tcc ttc gtg tcc ggg cag ctg tca gac agg ttt ggc agg      653
144 Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
145           155           160           165
146 aag aac gtt ctc ttc gca acc atg gct gta cag act ggc ttc agc ttc      701
147 Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
148 170           175           180           185
149 ctg cag att ttc tcc atc agc tgg gag atg ttc act gtg tta ttt gtc      749
150 Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
151           190           195           200
152 atc gtg ggc atg ggc cag atc tcc aac tat gtg gta gcc ttc ata cta      797
153 Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
154           205           210           215
155 gga aca gaa att ctt ggc aag tca gtt cgt att ata ttc tct aca tta      845

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156	Gly	Thr	Glu	Ile	Leu	Gly	Lys	Ser	Val	Arg	Ile	Ile	Phe	Ser	Thr	Leu	
157			220					225					230				
158	gga	gtg	tgc	aca	ttt	ttt	gca	gtt	ggc	tat	atg	ctg	ctg	cca	ctg	ttt	893
159	Gly	Val	Cys	Thr	Phe	Phe	Ala	Val	Gly	Tyr	Met	Leu	Leu	Pro	Leu	Phe	
160		235					240					245					
161	gct	tac	ttc	atc	aga	gac	tgg	cgg	atg	ctg	ctg	ctg	gcg	ctg	acg	gtg	941
162	Ala	Tyr	Phe	Ile	Arg	Asp	Trp	Arg	Met	Leu	Leu	Leu	Ala	Leu	Thr	Val	
163	250					255				260						265	
164	ccg	gga	gtg	ctg	tgt	gtc	ccg	ctg	tgg	tgg	ttc	att	cct	gaa	tct	ccc	989
165	Pro	Gly	Val	Leu	Cys	Val	Pro	Leu	Trp	Trp	Phe	Ile	Pro	Glu	Ser	Pro	
166				270					275						280		
167	cga	tgg	ctg	ata	tcc	cag	aga	aga	ttt	aga	gag	gct	gaa	gat	atc	atc	1037
168	Arg	Trp	Leu	Ile	Ser	Gln	Arg	Arg	Phe	Arg	Glu	Ala	Glu	Asp	Ile	Ile	
169				285					290					295			
170	caa	aaa	gct	gca	aaa	atg	aac	aac	aca	gct	gta	cca	gca	gtg	ata	ttt	1085
171	Gln	Lys	Ala	Ala	Lys	Met	Asn	Asn	Thr	Ala	Val	Pro	Ala	Val	Ile	Phe	
172		300						305					310				
173	gat	tct	gtg	gag	gag	cta	aat	ccc	ctg	aag	cag	cag	aaa	gct	ttc	att	1133
174	Asp	Ser	Val	Glu	Glu	Leu	Asn	Pro	Leu	Lys	Gln	Gln	Lys	Ala	Phe	Ile	
175		315				320					325						
176	ctg	gac	ctg	ttc	agg	act	cgg	aat	att	gcc	ata	atg	acc	att	atg	tct	1181
177	Leu	Asp	Leu	Phe	Arg	Thr	Arg	Asn	Ile	Ala	Ile	Met	Thr	Ile	Met	Ser	
178	330					335				340						345	
179	ttg	ctg	cta	tgg	atg	ctg	acc	tca	gtg	ggt	tac	ttt	gct	ctg	tct	ctg	1229
180	Leu	Leu	Leu	Trp	Met	Leu	Thr	Ser	Val	Gly	Tyr	Phe	Ala	Leu	Ser	Leu	
181				350					355						360		
182	gat	gct	cct	aat	tta	cat	gga	gat	gcc	tac	ctg	aac	tgt	ttc	ctc	tct	1277
183	Asp	Ala	Pro	Asn	Leu	His	Gly	Asp	Ala	Tyr	Leu	Asn	Cys	Phe	Leu	Ser	
184			365					370					375				
185	gcc	ttg	att	gaa	att	cca	gct	tac	att	aca	gcc	tgg	ctg	cta	ttg	cga	1325
186	Ala	Leu	Ile	Glu	Ile	Pro	Ala	Tyr	Ile	Thr	Ala	Trp	Leu	Leu	Leu	Arg	
187		380					385					390					
188	acg	ctg	ccc	agg	cgt	tat	atc	ata	gct	gca	gta	ctg	ttc	tgg	gga	gga	1373
189	Thr	Leu	Pro	Arg	Arg	Tyr	Ile	Ile	Ala	Ala	Val	Leu	Phe	Trp	Gly	Gly	
190		395				400					405						
191	ggt	gtg	ctt	ctc	ttc	att	caa	ctg	gta	cct	gtg	gat	tat	tac	ttc	tta	1421
192	Gly	Val	Leu	Leu	Phe	Ile	Gln	Leu	Val	Pro	Val	Asp	Tyr	Tyr	Phe	Leu	
193	410					415				420						425	
194	tcc	att	ggt	ctg	gtc	atg	ctg	gga	aaa	ttt	ggg	atc	acc	tct	gct	ttc	1469
195	Ser	Ile	Gly	Leu	Val	Met	Leu	Gly	Lys	Phe	Gly	Ile	Thr	Ser	Ala	Phe	
196			430						435						440		
197	tcc	atg	ctg	tat	gtc	ttc	act	gct	gag	ctc	tac	cca	acc	ctg	gtc	agg	1517
198	Ser	Met	Leu	Tyr	Val	Phe	Thr	Ala	Glu	Leu	Tyr	Pro	Thr	Leu	Val	Arg	
199			445						450					455			
200	aac	atg	gcg	gtg	ggg	gtc	aca	tcc	acg	gcc	tcc	aga	gtg	ggc	agc	atc	1565
201	Asn	Met	Ala	Val	Gly	Val	Thr	Ser	Thr	Ala	Ser	Arg	Val	Gly	Ser	Ile	
202		460						465					470				
203	att	gcc	ccc	tac	ttt	gtt	tac	ctc	ggt	gct	tac	aac	aga	atg	ctg	ccc	1613
204	Ile	Ala	Pro	Tyr	Phe	Val	Tyr	Leu	Gly	Ala	Tyr	Asn	Arg	Met	Leu	Pro	

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205      475      480      485
206 tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt      1661
207 Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
208 490      495      500      505
209 ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag      1709
210 Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
211      510      515      520
212 atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aaa aca aga gac tca      1757
213 Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
214      525      530      535
215 atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc      1799
216 Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
217      540      545      550
219 tgaaaaaata tctaccccat ttggtgaagt gaaaaacaga aaaataagac cctgtggaga      1859
220 aattcgttgt tcccactgaa atggactgac tgtaacgatt gacaccaaaa tgaaccttgc      1919
221 tatcaagaaa tgctcgtcat acagtaaact ctggatgatt cttccagata atgtccttgc      1979
222 ttacaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg      2039
223 taagatgtct tgaaaacatg ttagtcaagg actggtaaaa tacatataaa gattaacact      2099
224 cattccaat catacaaata ctatccaaat aaaaat      2135
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 557
228 <212> TYPE: PRT
229 <213> ORGANISM: Homo sapiens
231 <400> SEQUENCE: 3
232 Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
233 1      5      10      15
234 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
235      20      25      30
236 Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu His
237      35      40      45
238 Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn
239      50      55      60
240 His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His Ser
241 65      70      75      80
242 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly
243      85      90      95
244 Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser
245      100      105      110
246 Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Ile
247      115      120      125
248 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro Leu
249      130      135      140
250 Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile Ser
251 145      150      155      160
252 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val Thr
253      165      170      175
254 Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys Asn
255      180      185      190
256 Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln Ile

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 1,2,3,4,5,6,7,10,11,12,13,14

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 428
Seq#:6; Line(s) 439
Seq#:7; Line(s) 450
Seq#:8; Line(s) 461
Seq#:9; Line(s) 472
Seq#:10; Line(s) 483
Seq#:11; Line(s) 494
Seq#:12; Line(s) 505
Seq#:13; Line(s) 516
Seq#:14; Line(s) 527
Seq#:15; Line(s) 538
Seq#:16; Line(s) 549
Seq#:17; Line(s) 560
Seq#:18; Line(s) 571
Seq#:19; Line(s) 582
Seq#:20; Line(s) 593
Seq#:21; Line(s) 604
Seq#:24; Line(s) 815
Seq#:25; Line(s) 826
Seq#:26; Line(s) 837
Seq#:30; Line(s) 1057
Seq#:31; Line(s) 1068
Seq#:32; Line(s) 1079

VERIFICATION SUMMARY

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L:1092 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1096 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1100 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1104 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1108 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1112 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1116 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1120 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1124 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0